



STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/520,033
Source: PCT/10
Date Processed by STIC: 1/10/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. **EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)**
2. **U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314**

Revised 01/24/05



Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/520,033

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleic
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
- 5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 Skipped Sequences
(OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (ii) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8 Skipped Sequences
(NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/520,033

DATE: 01/10/2006
TIME: 08:16:21

Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\01102006\J520033.raw

3 <110> APPLICANT: Chan, Ragnel
 5 <120> TITLE OF INVENTION: Transcription factor gene induced by water deficit
 conditions and
 6 abscisic acid from Helianthus annuus, promoter and transgenic plants
 8 <130> FILE REFERENCE: US PCT
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/520,033
 C--> 10 <141> CURRENT FILING DATE: 2004-12-30
 10 <160> NUMBER OF SEQ ID NOS: 22
 12 <170> SOFTWARE: PatentIn version 3.1

see item 2 on Env summary sheet

These lines exceed 72 characters

see pp 1-6

ERRORED SEQUENCES

E--> 14 <210> *delete all alphabetical headings* *SEQ ID NO.1* *I ← just show 1* *Does Not Comply*
Corrected Diskette Needed
 15 <211> LENGTH: 774
 16 <212> TYPE: DNA
 17 <213> ORGANISM: Helianthus annuus
 OK > 19 <400> SEQUENCE: 1
 20 tcactagtac cataatattc acaaacacac acacctcaga aacgaagctt gcacataatg 60
 22 tctttcaac aagtacccac aacagaaaaca accaccagga agaacggaaa cgaggggcgg 120
 24 aaacgattta ccgacaaaca aataagttc cttagtaca tgtttgagac acagtcgaga 180
 26 cccgagttaa ggatgaaaca ccagttggca cataaactcg ggcttcatcc tcgtcaagtg 240
 28 gcgatatgg tccagaacaa acgcgcgcga tcaaagtctga ggcagattga gcaagagtat 300
 30 aacgcgctaa agcataacta cgagacgctt gcgtctaat ccgagtctct aaagaaagag 360
 32 aatcaggccc tactcaatca gttatgggtg caaaacttaca atgttgcatt caactattta 420
 34 agtagtttg aattttggta acaataaaga ttgacaaatg ttgtttgata attgattaac 480
 36 agttggaggt gctgagaaat gttagcagaaa agcatcaaga gaaaactagt agtagtggca 540
 38 gccgtgaaga atcggatgat cggtttacga actctccgga cgttatgtt ggtcaagaaa 600
 40 tgaatgtcc gtttgcgac gttttgcgt actttaaaga aggaaacagt ttgttggaga 660
 42 ttgaagaaca actgcgcagac cctcaaaagt ggtggagtt ctaaagagta aagaaggatg 720
 44 tagaagtagt agagtaaaaa ctaaaacata ccagatagtt ggtttacact ttgt 774
 E--> 47 <210> *SEQ ID NO.2*
 48 <211> LENGTH: 673
 49 <212> TYPE: DNA
 50 <213> ORGANISM: Helianthus annuus
 OK > 52 <400> SEQUENCE: 2
 53 tcactagtac cataatattc acaaacacac acacctcaga aacgaagctt gcacataatg 60
 55 tctttcaac aagtacccac aacagaaaaca accaccagga agaacggaaa cgaggggcgg 120
 57 aaacgattta ccgacaaaca aataagttc cttagtaca tgtttgagac acagtcgaga 180
 59 cccgagttaa ggatgaaaca ccagttggca cataaactcg ggcttcatcc tcgtcaagtg 240
 61 gcgatatgg tccagaacaa acgcgcgcga tcaaagtctga ggcagattga gcaagagtat 300
 63 aacgcgctaa agcataacta cgagacgctt gcgtctaat ccgagtctct aaagaaagag 360
 65 aatcaggccc tactcaatca gttggaggtg ctgagaaatg tagcagaaaa gcatcaagag 420
 67 aaaactagta gttagggcag cggtgaagaa tcggatgatc ggtttacgaa ctctccggac 480

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Input Set : A:\PTO.DA.txt
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69	gttatgtttg gtcaagaaaat gaatgttccg ttttgcgacg gttttgcgta ctttgaagaa	540
71	ggaaaacagtt tggtggagat tgaagaacaa ctgccagacc ctcaaaaagtg gtgggagttc	600
73	taaaagagtaa agaaggatgt agaagtagta gagtaaaaac taaaacatac cagatagttg	660
75	gtttacactt tgt	673

E--> 78 <210> SEQ_ID NO. 3

79 <211> LENGTH: 1221
80 <212> TYPE: DNA
81 <213> ORGANISM: Helianthus annuus
83 <220> FEATURE:
84 <221> NAME/KEY: promoter
85 <222> LOCATION: (1)..(1221)
86 <223> OTHER INFORMATION: Large allele

E--> 89 <400> SEQUENCE: 3

90	gatccaattt gaccacctgg cacatcgat cttatcttt ttgtcggttc caacacacca	60
92	caacacaccc acaaaacgtgt caattcacac ttccaccaatt tcatttcctt ttgtcaatc	120
94	atattaaaag tagtagcccc cacccccatt tgttacctac catttccac ttaataatc	180
96	accacacgcta tgtccacttg tacttttgt tgccacacaac tcttccata aaatatcaa	240
98	ccaaatttt ttttagtgaa aacaaattcc ccaaataaaaa tactaacgaa attcatcgca	300
100	tcagaataca ctcatctcg aacagtggcg aagcttgacg ttttcgacgg ggggtcgaa	360
102	aacgtatgta cccgaaattt ctatagaatc ggggggtcgaa aaacgtatata accaaaaatt	420
104	tctatacgaa aactacatata ataacactac tgagcaaaaa gttcgggggt tcgggcgccc	480
106	ctcccgcccc cttcaaaagct tcgccaatgt ctctgaaccg aaaaaaccc tcactcgct	540
108	actagccaat gaatccctac cagggaaacc ctcactcgtc ttactggact attggcgctt	600
110	ccaaatggac tacttgcgaa attcaccaca tcgggataca ctcgtctact gcgtgaggt	660
112	aaaacccgct tggctcaagg atcgaactag cgattgctgc ctactcgccat aatctccat	720
114	catcaacagg tgccgcccc aaaaaatgtc gggggcggga gttgaaccta ggtccagtga	780
116	cgcacccatg aattttttt ctaggatgc gaacgatgg tttaccata ctttaagag	840
118	gtgcgatcg aaattttacc tataaaatac actaaaaaaatggttccaaagggt ccacccaccc	900
120	cttaacctaa gtccgcctt gtctggatca cgtaaacat caggtctctc ccttaccagt	960
122	ccagctacga ctcattgaca aaatatcaaa accatatgt tttgagttt atctcaacccg	1020
124	aaagtgcacat catgacagag aatcgacata accaaaacgt gtaaacgtac aactcaccat	1080
126	tgcgtgaaa aggacaaaac aggtggatt cttgtcaat tcaacgcgta cacctgtgct	1140
128	tcatctaaac cccatacttt aagaacctt ataagacca ctcactatata atacacatata	1200
130	ataatatcac ttatcaaacc c	1221

E--> 133 <210> SEQ_ID NO. 4

134 <211> LENGTH: 28
135 <212> TYPE: DNA
136 <213> ORGANISM: Artificial
138 <220> FEATURE:
139 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter and having

Hind I

140 II site

E--> 142 <400> SEQUENCE: 4

143 gcgaagcttg atgcgaacga gtgggtta

28

E--> 146 <210> SEQ_ID NO. 5

147 <211> LENGTH: 28

148 <212> TYPE: DNA

149 <213> ORGANISM: Artificial

151 <220> FEATURE:

152 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter and having

Sal I

RAW SEQUENCE LISTING

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Input Set : A:\PTO.DA.txt

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153 site
 E-> 155 <400> SEQUENCE: 5 28
 156 gcggtcgaca cctggcacat cgtatctt
 E--> 159 <210> : SEQ_ID_NO.6
 160 <211> LENGTH: 27
 161 <212> TYPE: DNA
 162 <213> ORGANISM: Artificial
 164 <220> FEATURE:
 165 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter and having
 Bam HI
 166 site
 E-> 168 <400> SEQUENCE: 6 27
 169 cgcggatccg aqgggttgat aagtgat
 E--> 172 <210> SEQ_ID_NO.7
 173 <211> LENGTH: 27
 174 <212> TYPE: DNA
 175 <213> ORGANISM: Artificial
 177 <220> FEATURE:
 178 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter and having
 Hind I
 179 II site
 E-> 181 <400> SEQUENCE: 7 27
 182 cccaaagcta acctaaggccc gcctttg
 E--> 185 <210> SEQ_ID_NO.8
 186 <211> LENGTH: 27
 187 <212> TYPE: DNA
 188 <213> ORGANISM: Artificial
 190 <220> FEATURE:
 191 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter and having
 Hind II
 192 I site
 E-> 194 <400> SEQUENCE: 8 27
 195 ggcaagctta tctcaaccga aagtgac
 E--> 198 <210> SEQ_ID_NO.9
 199 <211> LENGTH: 19
 200 <212> TYPE: DNA
 201 <213> ORGANISM: Artificial
 203 <220> FEATURE:
 204 <223> OTHER INFORMATION: Designed oligonucleotide based on the 5' promoter
 E-> 206 <400> SEQUENCE: 9 19
 207 atttcgcaag tagtccatt
 E--> 210 <210> SEQ_ID_NO.10
 211 <211> LENGTH: 1015
 212 <212> TYPE: DNA
 213 <213> ORGANISM: Helianthus annuus
 E-> 215 <400> SEQUENCE: 10
 216 gatccaattt gaccacctgg cacatcgat cttatctctt ttgtcggttc caacacacca 60
 218 caacacaccc acaaactgtgt caattcacac ttcaccaatt tcatttcctt ttagtcaatc 120
 220 atattaaaag tagtagcccc caccccccatt tgtagccctac cattttccac ttataataatc 180
 222 acccacgcta tgtccacttg tactttgtt tgcacacacaac tcttccata aaatatcaaa 240
 224 ccaaattttt ttatggaa aacaaataact tcaaatgcac tattggtaa attcaccaca 300
 226 tcagaataca cccgtctcta ctcatctact ggccaaacggaa tcttcacggg ggaaaccctc 360

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Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\01102006\J520033.raw

228	actcgctcac	tgggactact	ggcgcttcaa	aatggactac	tgacaaaatt	caccacatcg	420
230	ggatacactt	gtctactgcg	gtgaggtaaa	atccgcccgt	cagctcaatg	atcgaactag	480
232	cgatcgccac	ccactcacct	tgtctcccat	catcaccagg	tgccgccaaa	acaaaatgtt	540
234	ggggcgaaaa	attgaaccta	ggtccagttt	cgcacccatg	aattttttt	ctagggatgc	600
236	gaacgagtga	tttaaccata	ctttaagag	gtgcgatcg	aaattttacc	tataaaatat	660
238	actaaaaaaaaa	tttcaagggt	ccgcccaccc	acccttaac	ctaagtccgc	ctctgcctgg	720
240	atcacgtgaa	acatcaggtc	tctctttac	cagttcacct	acaactcatt	gacaaaatata	780
242	caaaaccata	tgatttttag	ttttatctca	accgaaagtg	acatcatgac	agagaatcga	840
244	cataacccaa	acgtgtaaac	gtacaactca	ccattgcgtt	gaaaaggaca	aaacaggtag	900
246	gattcttgc	aaattcaacg	cgtacacctg	tgcttcatct	aaacccata	ctttaagaac	960
248	ctttataaaag	accactcaact	atatacac	atataataata	tcacttatca	aaccc	1015

E--> 251 <210> SEQ_ID_NO.11

252 <211> LENGTH: 28

253 <212> TYPE: DNA

254 <213> ORGANISM: Artificial

256 <220> FEATURE:

257 <223> OTHER INFORMATION: Designed oligonucleotide that matches nucleotides 81-100 of the H

258 ahb-4 cDNA sequence and having Bam HI site

E--> 260 <400> SEQUENCE: 11

261 ggcggatcca acagaaacaa ccaccagg

28

E--> 264 <210> SEQ_ID_NO.12

265 <211> LENGTH: 29

266 <212> TYPE: DNA

267 <213> ORGANISM: Artificial

269 <220> FEATURE:

270 <223> OTHER INFORMATION: Designed oligonucleotide for cloning 5' cDNA and having Bam HI s

271 ite

E--> 273 <400> SEQUENCE: 12

274 ggcggatccc ctqatggttt tttctgttg

29

E--> 277 <210> SEQ_ID_NO.13

278 <211> LENGTH: 34

279 <212> TYPE: DNA

280 <213> ORGANISM: Artificial

282 <220> FEATURE:

283 <223> OTHER INFORMATION: oligonucleotide based on 5' cDNA and having Xho I site

E--> 285 <400> SEQUENCE: 13

286 gaggactcga gctcaagttt tttttttttt tttt

34

E--> 289 <210> SEQ_ID_NO.14

290 <211> LENGTH: 18

291 <212> TYPE: DNA

292 <213> ORGANISM: Artificial

294 <220> FEATURE:

295 <223> OTHER INFORMATION: Oligonucleotide based on 5' cDNA and having Xho I site

E--> 297 <400> SEQUENCE: 14

298 gaggactcga gctcaagc

18

E--> 301 <210> SEQ_ID_NO.15

302 <211> LENGTH: 29

303 <212> TYPE: DNA

304 <213> ORGANISM: Artificial

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/520,033

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Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\01102006\J520033.raw

306 <220> FEATURE:
307 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter and having
Eco RI
308 site
E--> 310 <400> SEQUENCE: 15 29
311 gccgaattca gattgagcaa gagtataac
E--> 314 <210> ~~SEQ_ID_NO.16~~
315 <211> LENGTH: 19
316 <212> TYPE: DNA
317 <213> ORGANISM: Artificial
319 <220> FEATURE:
320 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter
E--> 322 <400> SEQUENCE: 16 19
323 acctttataaa agaccactc
E--> 326 <210> ~~SEQ_ID_NO.17~~
327 <211> LENGTH: 19
328 <212> TYPE: DNA
329 <213> ORGANISM: Artificial
331 <220> FEATURE:
332 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter
E--> 334 <400> SEQUENCE: 17 19
335 acgcaatgtt qaqttgtac
E--> 338 <210> ~~SEQ_ID_NO.18~~
339 <211> LENGTH: 24
340 <212> TYPE: DNA
341 <213> ORGANISM: Artificial
343 <220> FEATURE:
344 <223> OTHER INFORMATION: oligonucleotide to DNA-binding assays
E--> 346 <400> SEQUENCE: 18 24
347 aattcagatc tcaataattg agag
E--> 350 <210> ~~SEQ_ID_NO.19~~
351 <211> LENGTH: 24
352 <212> TYPE: DNA
353 <213> ORGANISM: Artificial
355 <220> FEATURE:
356 <223> OTHER INFORMATION: oligonucleotide to DNA-binding assays
E--> 358 <400> SEQUENCE: 19 24
359 gatcctctca attattggaga tctg
E--> 362 <210> ~~SEQ_ID_NO.20~~
363 <211> LENGTH: 30
364 <212> TYPE: DNA
365 <213> ORGANISM: Artificial
367 <220> FEATURE:
368 <223> OTHER INFORMATION: Oligonucleotide having Bam HI site
E--> 370 <400> SEQUENCE: 20 30
371 gcgggatcca ccatgtctct tcaacaagta
E--> 374 <210> ~~SEQ_ID_NO.21~~
375 <211> LENGTH: 30
376 <212> TYPE: DNA
377 <213> ORGANISM: Artificial

RAW SEQUENCE LISTING

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Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\01102006\J520033.raw

379 <220> FEATURE:

380 <223> OTHER INFORMATION: Oligonucleotide having Sac I site

E--> 382 <400> SEQUENCE: 21

383 gccgagctct tagaactcca accactttg

30

E--> 386 <210> ~~SEQ-ID NO. 22~~

387 <211> LENGTH: 27

388 <212> TYPE: DNA

389 <213> ORGANISM: Artificial

391 <220> FEATURE:

392 <223> OTHER INFORMATION: Oligonucleotide having Bam HI site

E--> 394 <400> SEQUENCE: 22

395 ggcggatccg tctccagtt gtttttc

27

E--> 398 7

delete

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/520,033

DATE: 01/10/2006
TIME: 08:16:22

Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\01102006\J520033.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:14 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:19 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:1
L:47 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:52 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:2
L:78 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:89 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:3
L:133 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:142 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:4
L:146 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:155 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:5
L:159 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:168 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:6
L:172 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:181 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:7
L:185 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:194 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:8
L:198 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:206 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:9
L:210 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:215 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:10
L:251 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:260 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:11
L:264 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:273 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:12
L:277 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:285 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:13
L:289 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:297 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:14
L:301 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:310 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:15
L:314 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:322 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:16
L:326 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:334 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:17
L:338 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:346 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:18
L:350 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:358 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:19
L:362 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:370 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:20
L:374 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:382 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:21
L:386 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:394 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:22
L:398 M:254 E: No. of Bases conflict, this line has no nucleotides.